

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/577,008
Source: 1 FWD
Date Processed by STIC: 1/19/07

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RAW SEQUENCE LISTING

DATE: 01/19/2007

PATENT APPLICATION: US/10/577,008

TIME: 16:40:54

Input Set : A:\2007-01-11 3749-0112PUS1.txt

Output Set: N:\CRF4\01192007\J577008.raw

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3 <110> APPLICANT: SUZUKI, Toshiharu et al.
5 <120> TITLE OF INVENTION: MARKER PEPTIDE FOR ALZHEIMER'S DISEASE
7 <130> FILE REFERENCE: 3749-0112PUS1
9 <140> CURRENT APPLICATION NUMBER: US 10/577,008
10 <141> CURRENT FILING DATE: 2006-04-25
12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/016209
13 <151> PRIOR FILING DATE: 2004-11-01
15 <150> PRIOR APPLICATION NUMBER: JP 2003/375363
16 <151> PRIOR FILING DATE: 2003-11-05
18 <160> NUMBER OF SEQ ID NOS: 13
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 971
24 <212> TYPE: PRT
25 <213> ORGANISM: human
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31 Leu Ala Gly Leu Leu Cys Gly Gly Gly Val Trp Ala Ala Arg Val Asn
32           20           25           30
34 Lys His Lys Pro Trp Leu Glu Pro Thr Tyr His Gly Ile Val Thr Glu
35           35           40           45
37 Asn Asp Asn Thr Val Leu Leu Asp Pro Pro Leu Ile Ala Leu Asp Lys
38           50           55           60
40 Asp Ala Pro Leu Arg Phe Ala Gly Glu Ile Cys Gly Phe Lys Ile His
41   65           70           75           80
43 Gly Gln Asn Val Pro Phe Asp Ala Val Val Val Asp Lys Ser Thr Gly
44           85           90           95
46 Glu Gly Val Ile Arg Ser Lys Glu Lys Leu Asp Cys Glu Leu Gln Lys
47           100          105          110
49 Asp Tyr Ser Phe Thr Ile Gln Ala Tyr Asp Cys Gly Lys Gly Pro Asp
50           115          120          125
52 Gly Thr Asn Val Lys Lys Ser His Lys Ala Thr Val His Ile Gln Val
53           130          135          140
55 Asn Asp Val Asn Glu Tyr Ala Pro Val Phe Lys Glu Lys Ser Tyr Lys
56 145          150          155          160
58 Ala Thr Val Ile Glu Gly Lys Gln Tyr Asp Ser Ile Leu Arg Val Glu
59           165          170          175
61 Ala Val Asp Ala Asp Cys Ser Pro Gln Phe Ser Gln Ile Cys Ser Tyr
62           180          185          190
64 Glu Ile Ile Thr Pro Asp Val Pro Phe Thr Val Asp Lys Asp Gly Tyr
65           195          200          205
67 Ile Lys Asn Thr Glu Lys Leu Asn Tyr Gly Lys Glu His Gln Tyr Lys

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68      210      215      220
70 Leu Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala Thr Glu Asp
71 225      230      235      240
73 Val Leu Val Lys Ile Ser Ile Lys Pro Thr Cys Thr Pro Gly Trp Gln
74      245      250      255
76 Gly Trp Asn Asn Arg Ile Glu Tyr Glu Pro Gly Thr Gly Ala Leu Ala
77      260      265      270
79 Val Phe Pro Asn Ile His Leu Glu Thr Cys Asp Glu Pro Val Ala Ser
80      275      280      285
82 Val Gln Ala Thr Val Glu Leu Glu Thr Ser His Ile Gly Lys Gly Cys
83      290      295      300
85 Asp Arg Asp Thr Tyr Ser Glu Lys Ser Leu His Arg Leu Cys Gly Ala
86 305      310      315      320
88 Ala Ala Gly Thr Ala Glu Leu Leu Pro Ser Pro Ser Gly Ser Leu Asn
89      325      330      335
91 Trp Thr Met Gly Leu Pro Thr Asp Asn Gly His Asp Ser Asp Gln Val
92      340      345      350
94 Phe Glu Phe Asn Gly Thr Gln Ala Val Arg Ile Pro Asp Gly Val Val
95      355      360      365
97 Ser Val Ser Pro Lys Glu Pro Phe Thr Ile Ser Val Trp Met Arg His
98      370      375      380
100 Gly Pro Phe Gly Arg Lys Lys Glu Thr Ile Leu Cys Ser Ser Asp Lys
101 385      390      395      400
103 Thr Asp Met Asn Arg His His Tyr Ser Leu Tyr Val His Gly Cys Arg
104      405      410      415
106 Leu Ile Phe Leu Phe Arg Gln Asp Pro Ser Glu Glu Lys Lys Tyr Arg
107      420      425      430
109 Pro Ala Glu Phe His Trp Lys Leu Asn Gln Val Cys Asp Glu Glu Trp
110      435      440      445
112 His His Tyr Val Leu Asn Val Glu Phe Pro Ser Val Thr Leu Tyr Val
113      450      455      460
115 Asp Gly Thr Ser His Glu Pro Phe Ser Val Thr Glu Asp Tyr Pro Leu
116 465      470      475      480
118 His Pro Ser Lys Ile Glu Thr Gln Leu Val Val Gly Ala Cys Trp Gln
119      485      490      495
121 Glu Phe Ser Gly Val Glu Asn Asp Asn Glu Thr Glu Pro Val Thr Val
122      500      505      510
124 Ala Ser Ala Gly Gly Asp Leu His Met Thr Gln Phe Phe Arg Gly Asn
125      515      520      525
127 Leu Ala Gly Leu Thr Leu Arg Ser Gly Lys Leu Ala Asp Lys Lys Val
128      530      535      540
130 Ile Asp Cys Leu Tyr Thr Cys Lys Glu Gly Leu Asp Leu Gln Val Leu
131 545      550      555      560
133 Glu Asp Ser Gly Arg Gly Val Gln Ile Gln Ala His Pro Ser Gln Leu
134      565      570      575
136 Val Leu Thr Leu Glu Gly Glu Asp Leu Gly Glu Leu Asp Lys Ala Met
137      580      585      590
139 Gln His Ile Ser Tyr Leu Asn Ser Arg Gln Phe Pro Thr Pro Gly Ile
140      595      600      605

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142 Arg Arg Leu Lys Ile Thr Ser Thr Ile Lys Cys Phe Asn Glu Ala Thr
143      610                      615                      620
145 Cys Ile Ser Val Pro Pro Val Asp Gly Tyr Val Met Val Leu Gln Pro
146 625                      630                      635                      640
148 Glu Glu Pro Lys Ile Ser Leu Ser Gly Val His His Phe Ala Arg Ala
149      645                      650                      655
151 Ala Ser Glu Phe Glu Ser Ser Glu Gly Val Phe Leu Phe Pro Glu Leu
152      660                      665                      670
154 Arg Ile Ile Ser Thr Ile Thr Arg Glu Val Glu Pro Glu Gly Asp Gly
155      675                      680                      685
157 Ala Glu Asp Pro Thr Val Gln Glu Ser Leu Val Ser Glu Glu Ile Val
158      690                      695                      700
160 His Asp Leu Asp Thr Cys Glu Val Thr Val Glu Gly Glu Glu Leu Asn
161 705                      710                      715                      720
163 His Glu Gln Glu Ser Leu Glu Val Asp Met Ala Arg Leu Gln Gln Lys
164      725                      730                      735
166 Gly Ile Glu Val Ser Ser Ser Glu Leu Gly Met Thr Phe Thr Gly Val
167      740                      745                      750
169 Asp Thr Met Ala Ser Tyr Glu Glu Val Leu His Leu Leu Arg Tyr Arg
170      755                      760                      765
172 Asn Trp His Ala Arg Ser Leu Leu Asp Arg Lys Phe Lys Leu Ile Cys
173      770                      775                      780
175 Ser Glu Leu Asn Gly Arg Tyr Ile Ser Asn Glu Phe Lys Val Glu Val
176 785                      790                      795                      800
178 Asn Val Ile His Thr Ala Asn Pro Met Glu His Ala Asn His Met Ala
179      805                      810                      815
181 Ala Gln Pro Gln Phe Val His Pro Glu His Arg Ser Phe Val Asp Leu
182      820                      825                      830
184 Ser Gly His Asn Leu Ala Asn Pro His Pro Phe Ala Val Val Pro Ser
185      835                      840                      845
187 Thr Ala Thr Val Val Ile Val Val Cys Val Ser Phe Leu Val Phe Met
188      850                      855                      860
190 Ile Ile Leu Gly Val Phe Arg Ile Arg Ala Ala His Arg Arg Thr Met
191 865                      870                      875                      880
193 Arg Asp Gln Asp Thr Gly Lys Glu Asn Glu Met Asp Trp Asp Asp Ser
194      885                      890                      895
196 Ala Leu Thr Ile Thr Val Asn Pro Met Glu Thr Tyr Glu Asp Gln His
197      900                      905                      910
199 Ser Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Ser Glu Asp
200      915                      920                      925
202 Gly Glu Glu Glu Asp Asp Ile Thr Ser Ala Glu Ser Glu Ser Ser Glu
203      930                      935                      940
205 Glu Glu Glu Gly Glu Gln Gly Asp Pro Gln Asn Ala Thr Arg Gln Gln
206 945                      950                      955                      960
208 Gln Leu Glu Trp Asp Asp Ser Thr Leu Ser Tyr
209      965                      970
211 <210> SEQ ID NO: 2
212 <211> LENGTH: 968
213 <212> TYPE: PRT

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Output Set: N:\CRF4\01192007\J577008.raw

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214 <213> ORGANISM: human
216 <400> SEQUENCE: 2
217 Met Val Leu Gly Cys Glu Leu Ser Gly Ser Thr Arg Val Val Val Gly
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220 Val Glu Ala Leu Leu Thr Gly Ala Ser Ser Pro Leu Pro Gly Val Gly
221           20           25           30
223 Pro Ala Asn Lys His Lys Pro Trp Ile Glu Ala Glu Tyr Gln Gly Ile
224           35           40           45
226 Val Met Glu Asn Asp Asn Thr Val Leu Leu Asn Pro Pro Leu Phe Ala
227           50           55           60
229 Leu Asp Lys Asp Ala Pro Leu Arg Tyr Ala Gly Glu Ile Cys Gly Phe
230           65           70           75           80
232 Arg Leu His Gly Ser Gly Val Pro Phe Glu Ala Val Ile Leu Asp Lys
233           85           90           95
235 Ala Thr Gly Glu Gly Leu Ile Arg Ala Lys Glu Pro Val Asp Cys Glu
236           100          105          110
238 Ala Gln Lys Glu His Thr Phe Thr Ile Gln Ala Tyr Asp Cys Gly Glu
239           115          120          125
241 Gly Pro Asp Gly Ala Asn Thr Lys Lys Ser His Lys Ala Thr Val His
242           130          135          140
244 Val Arg Val Asn Asp Val Asn Glu Phe Ala Pro Val Phe Val Glu Arg
245           145          150          155          160
247 Leu Tyr Arg Ala Ala Val Thr Glu Gly Lys Leu Tyr Asp Arg Ile Leu
248           165          170          175
250 Arg Val Glu Ala Ile Asp Gly Asp Cys Ser Pro Gln Tyr Ser Gln Ile
251           180          185          190
253 Cys Tyr Tyr Glu Ile Leu Thr Pro Asn Thr Pro Phe Leu Ile Asp Asn
254           195          200          205
256 Asp Gly Asn Ile Glu Asn Thr Glu Lys Leu Gln Tyr Ser Gly Glu Arg
257           210          215          220
259 Leu Tyr Lys Phe Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala
260           225          230          235          240
262 Ala Asp Asp Ala Glu Val Glu Ile Gln Val Lys Pro Thr Cys Lys Pro
263           245          250          255
265 Ser Trp Gln Gly Trp Asn Lys Arg Ile Glu Tyr Ala Pro Gly Ala Gly
266           260          265          270
268 Ser Leu Ala Leu Phe Pro Gly Ile Arg Leu Glu Thr Cys Asp Glu Pro
269           275          280          285
271 Leu Trp Asn Ile Gln Ala Thr Ile Glu Leu Gln Thr Ser His Val Ala
272           290          295          300
274 Lys Gly Cys Asp Arg Asp Asn Tyr Ser Glu Arg Ala Leu Arg Lys Leu
275           305          310          315          320
277 Cys Gly Ala Ala Thr Gly Glu Val Asp Leu Leu Pro Met Pro Gly Pro
278           325          330          335
280 Asn Ala Asn Trp Thr Ala Gly Leu Ser Val His Tyr Ser Gln Asp Ser
281           340          345          350
283 Ser Leu Ile Tyr Trp Phe Asn Gly Thr Gln Ala Val Gln Val Pro Leu
284           355          360          365
286 Gly Gly Pro Ser Gly Leu Gly Ser Gly Pro Gln Asp Ser Leu Ser Asp

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287      370      375      380
289 His Phe Thr Leu Ser Phe Trp Met Lys His Gly Val Thr Pro Asn Lys
290 385      390      395      400
292 Gly Lys Lys Glu Glu Glu Thr Ile Val Cys Asn Thr Val Gln Asn Glu
293      405      410      415
295 Asp Gly Phe Ser His Tyr Ser Leu Thr Val His Gly Cys Arg Ile Ala
296      420      425      430
298 Phe Leu Tyr Trp Pro Leu Leu Glu Ser Ala Arg Pro Val Lys Phe Leu
299      435      440      445
301 Trp Lys Leu Glu Gln Val Cys Asp Asp Glu Trp His His Tyr Ala Leu
302      450      455      460
304 Asn Leu Glu Phe Pro Thr Val Thr Leu Tyr Thr Asp Gly Ile Ser Phe
305 465      470      475      480
307 Asp Pro Ala Leu Ile His Asp Asn Gly Leu Ile His Pro Pro Arg Arg
308      485      490      495
310 Glu Pro Ala Leu Met Ile Gly Ala Cys Trp Thr Glu Glu Lys Asn Lys
311      500      505      510
313 Glu Lys Glu Lys Gly Asp Asn Ser Thr Asp Thr Thr Gln Gly Asp Pro
314      515      520      525
316 Leu Ser Ile His His Tyr Phe His Gly Tyr Leu Ala Gly Phe Ser Val
317      530      535      540
319 Arg Ser Gly Arg Leu Glu Ser Arg Glu Val Ile Glu Cys Leu Tyr Ala
320 545      550      555      560
322 Cys Arg Glu Gly Leu Asp Tyr Arg Asp Phe Glu Ser Leu Gly Lys Gly
323      565      570      575
325 Met Lys Val His Val Asn Pro Ser Gln Ser Leu Leu Thr Leu Glu Gly
326      580      585      590
328 Asp Asp Val Glu Thr Phe Asn His Ala Leu Gln His Val Ala Tyr Met
329      595      600      605
331 Asn Thr Leu Arg Phe Ala Thr Pro Gly Val Arg Pro Leu Arg Leu Thr
332      610      615      620
334 Thr Ala Val Lys Cys Phe Ser Glu Glu Ser Cys Val Ser Ile Pro Glu
335 625      630      635      640
337 Val Glu Gly Tyr Val Val Val Leu Gln Pro Asp Ala Pro Gln Ile Leu
338      645      650      655
340 Leu Ser Gly Thr Ala His Phe Ala Arg Pro Ala Val Asp Phe Glu Gly
341      660      665      670
343 Thr Asn Gly Val Pro Leu Phe Pro Asp Leu Gln Ile Thr Cys Ser Ile
344      675      680      685
346 Ser His Gln Val Glu Ala Lys Lys Asp Glu Ser Trp Gln Gly Thr Val
347      690      695      700
349 Thr Asp Thr Arg Met Ser Asp Glu Ile Val His Asn Leu Asp Gly Cys
350 705      710      715      720
352 Glu Ile Ser Leu Val Gly Asp Asp Leu Asp Pro Glu Arg Glu Ser Leu
353      725      730      735
355 Leu Leu Asp Thr Thr Ser Leu Gln Gln Arg Gly Leu Glu Leu Thr Asn
356      740      745      750
358 Thr Ser Ala Tyr Leu Thr Ile Ala Gly Val Glu Ser Ile Thr Val Tyr
359      755      760      765

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VERIFICATION SUMMARY

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